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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/080,210

DATE: 03/11/2002
TIME: 10:42:16

Input Set : A:\GC561-3-SEQLIST.TXT
Output Set: N:\CRF3\03112002\J080210.raw

4 <110> APPLICANT: Wang, Huaming
5 Bodie, Elizabeth A.
7 <120> TITLE OF INVENTION: Phenol Oxidizing Enzymes
10 <130> FILE REFERENCE: GC561-3
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/080,210
C--> 13 <141> CURRENT FILING DATE: 2002-02-19
15 <150> PRIOR APPLICATION NUMBER: US 09/220,871
16 <151> PRIOR FILING DATE: 1998-12-23
18 <150> PRIOR APPLICATION NUMBER: US 09/338,723
19 <151> PRIOR FILING DATE: 1999-06-23
21 <160> NUMBER OF SEQ ID NOS: 17
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 3677
27 <212> TYPE: DNA
28 <213> ORGANISM: Stachybotrys chartarum
30 <400> SEQUENCE: 1

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32 agtcaatatac ttggtcactg ctaatagttc cttgtctacgc gcaaaaagct ccttgccgaa      120
33 ggggcacaga ctatcaagtg agacatatag gatgcatgtc ttctatagcc acagttaggg      180
34 tgggtgacctc atcgaagagg ccccgacttg catgcatacg acatgtcgct tccatgcaac      240
35 atgtatgcgc acatcggcga tcaggcacc cctgcatgca gaatagaacc cccctggttt      300
36 cctttttgttt cttttccttt ctcaacgacg cgtgagcgtg gttaacttga gcaaggccga      360
37 gtggtctgtt cagcagggtta ccatcgaaact ctcttctttt ccaatcatga cctgcccccc      420
38 gaggtttagcc cccatcacgg ctgtgaaatc cacttcgata atcctagcct agtgctactc      480
39 ttcaatagtt gctcctgatg gggcactttg gtcacattgc cttggtttct cctacctcgt      540
40 tctcttccgc atcaagcctc tatgcccgcg gacaacacct cattggcccg gaccactttg      600
41 agcgcgcacg cacttccgcg ccgaaggagt tgataacacc cttcaccctt gcccaatgat      660
42 ggagttttgg tctatttgtc atgatccact cacattcact agatcacgga tccctggaaga      720
43 ggggtgtggaa gccagaccag cttgtccctg ttcttgcaga ctcaggtcag ctccctagcgg      780
44 ctatcacagc tcaggattat caagtccegt aaagtccaga ccccttttcat tgtatgatgc      840
45 tgcctaattt gcgctatctc tatgcccgtg cagccgtctt ggctacaact ggctgccatg      900
46 gctgaagcat cgtgagatct ataaaggctc ccgaatcctc ggtgaagtca gaatcgtctc      960
47 tccacaccag tcaacaacaa gcttctttct cttacagctt agcctgagca cattcacaga      1020
48 actcttccct tcttttctgc aatatgctgt tcaagtcata gcaactggca gcagcctccg      1080
49 ggctcctgtc tggagtcctc ggcataccga tggacaccgg cagccacccc attgaggctg      1140
50 ttgatcccgga agtgaagact gaggtcttcg ctgactccct ccttgctgca gcaggcgatg      1200
51 acgactggga gtcacctcca tacaacttgc ttacagggtg agacacctgt cccacctgtt      1260
52 ttcctctgat aactaactct tataggaatg cccctgccaat tccacctgtc aagcagccca      1320
53 agatgtatgt ctttgatttt ctacgaagca actcggcccc gactaatgta ttctaggatc      1380
54 attaccaacc ctgtcaccgg caaggacatt tgggtactatg agatcgagat caagccattt      1440
55 cagcaaaggg tgagtttgct cagaaacctt gtggtaatta atcattgtta ctgacccttt      1500
56 cagattttacc ccacttgcg cccctgccact ctgcctggct acgatggcat gagccctggt      1560

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57 cctactttca atgttcccag aggaacagag actgtagtta ggttcatcaa caatgccacc 1620
58 gtggagaact cgggtccatct gcacggctcc ccatcgctg cccctttcga tgggtgggct 1680
59 gaagatgtga ccttccctgg cgagtacaag gattactact ttcccaacta ccaatccgcc 1740
60 cgccttctgt ggtaccatga ccacgctttc atgaaggat gctacgagcc tttatctttc 1800
61 ttggctacct ttggctaacc aacttccctt cgtagactgc tgagaatgcc tactttggtc 1860
62 aggctggcgc ctacattatc aacgacgagg ctgaggatgc tctcggtctt cctagtggct 1920
63 atggcgagtt cgatatccct ctgactctga cggccaagta ctataacgcc gatggtaccc 1980
64 tgcgttcgac cgagggtgag gaccaggacc tgtggggaga tgtcatccat gtcaacggac 2040
65 agccatggcc ttctctaac gtccagcccc gcaagtaccg ttcccgattc ctcaacgctg 2100
66 cegtgtctcg tcttggctc ctctacctcg tcaggaccag ctctcccaac gtcagaattc 2160
67 ctttccaagt cattgctctt gatgtctgtc tccttcaagc ccccgttcag acctctaacc 2220
68 tctaccttgc tgttgccgag cgttaacgaga tcattatttg tatgcccctc cctctcacga 2280
69 atgagtcagg aactctaaga ctaacacttg tagacttcac caactttgct ggccagactc 2340
70 ttgacctgcg caacgttctt gagaccaacg atgtcggcga cgaggatgag tacgctcgca 2400
71 ctctcgaggt gatgcgcttc gtctcagct ctggcactgt tgaggacaac agccaggctc 2460
72 cctccactct ccgtgacgtt cctttccctc ctcaacaagg aggcccgcc gacaagcact 2520
73 tcaagtttga acgcagcaac ggacactacc tgatcaacga tgttggcttt gccgatgtca 2580
74 atgagcgtgt cctggccaag cccgagctcg gcaccgttga ggtctgggag ctcgagaact 2640
75 cctctggagg ctggagccac cccgtccaca ttaccttg tgaactcaag atcctcaagc 2700
76 gaactggtgg tctgtggccg gtcatgccct acgagctctg tggctttaag gatgtcgtct 2760
77 ggttgggcag ggggtgagac ctgaccatcg aggccacta ccaaccctgg actggagctt 2820
78 acatgtggca ctgtcacaac ctcattcacg aggataacga catgatggct gtattcaacg 2880
79 tcaccgccat ggaggagaag ggatatcttc agaggactt cgaggacccc atgaacccca 2940
80 agtggcgcgc cgttccctac aaccgcaacg acttccatgc tcgcgctgga aacttctccg 3000
81 ccgagtcctt cactgcccga gtgcaggagc tggccgagca ggagccgtac aaccgcctcg 3060
82 atgagatcct ggaggatctt ggaatcgagg agtaaaccce gagccacaag ctctacaatc 3120
83 gttttgagtc ttaagaacgag gctcttgggt cgtattcttt tcttccctac ggggaactcc 3180
84 gctgtccact gcgatgtgaa ggaccatcac aaagcaacgt atatatgga ctaccactg 3240
85 tcattaccgc ccacttgtac ctattcgatt cttgttcaaa cttttctagt gcgagagtgt 3300
86 ccatagtcaa gaaacgcca tagggctatc gtctaaactg aactattgtg tggctctgtg 3360
87 cgtggagtag atgtcaattg tgatgagaca cagtaaatac ggtatatctt ttctaggac 3420
88 tacaggatca gtttctcatg agattacatc cgtctaattg ttgtccatga gagtctagct 3480
89 aaggttgaga atgcacaga cggaaatcatt tgatgctctc agctcgtatt accgatgtaa 3540
90 gacaagttag gtaagttgct tggtatccga aaatgactca ggctccctca ttaggttgca 3600
91 tgtgaaaacc ttcagcaact catgggtgtt gggaccaaat catccatacc tgattttgat 3660
92 aactgacctg ggtcaat 3677

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94 <210> SEQ ID NO: 2

95 <211> LENGTH: 594

96 <212> TYPE: PRT

97 <213> ORGANISM: *Stachybotrys chartarum*

99 <400> SEQUENCE: 2

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100 Met Leu Phe Lys Ser Trp Gln Leu Ala Ala Ala Ser Gly Leu Leu Ser
101 1 5 10 15
102 Gly Val Leu Gly Ile Pro Met Asp Thr Gly Ser His Pro Ile Glu Ala
103 20 25 30
104 Val Asp Pro Glu Val Lys Thr Glu Val Phe Ala Asp Ser Leu Leu Ala
105 35 40 45
106 Ala Ala Gly Asp Asp Asp Trp Glu Ser Pro Pro Tyr Asn Leu Leu Tyr
107 50 55 60

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108 Arg Asn Ala Leu Pro Ile Pro Pro Val Lys Gln Pro Lys Met Ile Ile
109 65 70 75 80
110 Thr Asn Pro Val Thr Gly Lys Asp Ile Trp Tyr Tyr Glu Ile Glu Ile
111 85 90 95
112 Lys Pro Phe Gln Gln Arg Ile Tyr Pro Thr Leu Arg Pro Ala Thr Leu
113 100 105 110
114 Val Gly Tyr Asp Gly Met Ser Pro Gly Pro Thr Phe Asn Val Pro Arg
115 115 120 125
116 Gly Thr Glu Thr Val Val Arg Phe Ile Asn Asn Ala Thr Val Glu Asn
117 130 135 140
118 Ser Val His Leu His Gly Ser Pro Ser Arg Ala Pro Phe Asp Gly Trp
119 145 150 155 160
120 Ala Glu Asp Val Thr Phe Pro Gly Glu Tyr Lys Asp Tyr Tyr Phe Pro
121 165 170 175
122 Asn Tyr Gln Ser Ala Arg Leu Leu Trp Tyr His Asp His Ala Phe Met
123 180 185 190
124 Lys Thr Ala Glu Asn Ala Tyr Phe Gly Gln Ala Gly Ala Tyr Ile Ile
125 195 200 205
126 Asn Asp Glu Ala Glu Asp Ala Leu Gly Leu Pro Ser Gly Tyr Gly Glu
127 210 215 220
128 Phe Asp Ile Pro Leu Ile Leu Thr Ala Lys Tyr Tyr Asn Ala Asp Gly
129 225 230 235 240
130 Thr Leu Arg Ser Thr Glu Gly Glu Asp Gln Asp Leu Trp Gly Asp Val
131 245 250 255
132 Ile His Val Asn Gly Gln Pro Trp Pro Phe Leu Asn Val Gln Pro Arg
133 260 265 270
134 Lys Tyr Arg Phe Arg Phe Leu Asn Ala Ala Val Ser Arg Ala Trp Leu
135 275 280 285
136 Leu Tyr Leu Val Arg Thr Ser Ser Pro Asn Val Arg Ile Pro Phe Gln
137 290 295 300
138 Val Ile Ala Ser Asp Ala Gly Leu Leu Gln Ala Pro Val Gln Thr Ser
139 305 310 315 320
140 Asn Leu Tyr Leu Ala Val Ala Glu Arg Tyr Glu Ile Ile Ile Asp Phe
141 325 330 335
142 Thr Asn Phe Ala Gly Gln Thr Leu Asp Leu Arg Asn Val Ala Glu Thr
143 340 345 350
144 Asn Asp Val Gly Asp Glu Asp Glu Tyr Ala Arg Thr Leu Glu Val Met
145 355 360 365
146 Arg Phe Val Val Ser Ser Gly Thr Val Glu Asp Asn Ser Gln Val Pro
147 370 375 380
148 Ser Thr Leu Arg Asp Val Pro Phe Pro Pro His Lys Glu Gly Pro Ala
149 385 390 395 400
150 Asp Lys His Phe Lys Phe Glu Arg Ser Asn Gly His Tyr Leu Ile Asn
151 405 410 415
152 Asp Val Gly Phe Ala Asp Val Asn Glu Arg Val Leu Ala Lys Pro Glu
153 420 425 430
154 Leu Gly Thr Val Glu Val Trp Glu Leu Glu Asn Ser Ser Gly Gly Trp
155 435 440 445
156 Ser His Pro Val His Ile His Leu Val Asp Phe Lys Ile Leu Lys Arg

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157      450      455      460
158 Thr Gly Gly Arg Gly Gln Val Met Pro Tyr Glu Ser Ala Gly Leu Lys
159 465      470      475      480
160 Asp Val Val Trp Leu Gly Arg Gly Glu Thr Leu Thr Ile Glu Ala His
161      485      490      495
162 Tyr Gln Pro Trp Thr Gly Ala Tyr Met Trp His Cys His Asn Leu Ile
163      500      505      510
164 His Glu Asp Asn Asp Met Met Ala Val Phe Asn Val Thr Ala Met Glu
165      515      520      525
166 Glu Lys Gly Tyr Leu Gln Glu Asp Phe Glu Asp Pro Met Asn Pro Lys
167      530      535      540
168 Trp Arg Ala Val Pro Tyr Asn Arg Asn Asp Phe His Ala Arg Ala Gly
169 545      550      555      560
170 Asn Phe Ser Ala Glu Ser Ile Thr Ala Arg Val Gln Glu Leu Ala Glu
171      565      570      575
172 Gln Glu Pro Tyr Asn Arg Leu Asp Glu Ile Leu Glu Asp Leu Gly Ile
173      580      585      590
174 Glu Glu
177 <210> SEQ ID NO: 3
178 <211> LENGTH: 2905
179 <212> TYPE: DNA
180 <213> ORGANISM: Bipolaris spicifera
182 <400> SEQUENCE: 3
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184 aatcccatca tcagcttttg aacattctca gctcatcaaa gattttcttc aagatggtcg 120
185 ccaaataacct cttctcagca cttcaactcg ttccaattgc gaaaggcata tacggygtcg 180
186 ctttgagcga acgtcccgcc aaatttgctg acaacacccc cgacgaagaa aaggctgcct 240
187 tggcgctcaat tgttgaagat gacctgctcg atgttgctca catgctgaaa gactggcaaa 300
188 gcccgagata tcctctcatt ttctgcacac cactgcccac cctccagcc aaggaaccaa 360
189 aqtagttagt gttcaatcgc atcgacaggt ttcttagaat atactacca tccacagtaa 420
190 actcacgaat cctgtcacaa acaaggagat atggtactac gagattgtca tcaaaccctt 480
191 caccagcagc gtctatccaa gctgctgccc tgctcgctta gtaggctatg acggcatctc 540
192 cccaggtcct acgatcatag tgcgagaggg aacagaagct gttgtacggg ttataaacca 600
193 gqgtgatcgc gaaagctcca tccatctcca cggctcccc tcccggtccc cttttgacgg 660
194 atgggctgat gatatgatca tgaaggggga atacaaaggt acgatagcgt gtgattctac 720
195 gcatcaggaa gcctctatca tactaacagg actttcttct cagactacta ctaccgaac 780
196 aaccaagctg ccagattttt gtggtaccac gatcatgcta tgcattgtgt aagtctttac 840
197 cgaactttta tggtagtgaa acggaaggat taagetaaca tctgtgcaga ccgcagaaaa 900
198 tgctattttc gggcaagccg gcgcctacct gatcacagac ccggtgagg atgctctcgg 960
199 ccttccttca ggttacggaa aatacgacat tccgctgggt ctcagttcca agtactacaa 1020
200 cgcgatgga actcttaaga ccagtgtggg agaagacaag agtgtttggg gcgacatcat 1080
201 ccattgtcaac ggtcagccct ggccattctt aaatgttgag cctcgaaagt atcgtcttcg 1140
202 attcctcaac gcgctgtttt ctaggaaact tgccctttac ttcgtcaagc aagacaacac 1200
203 tgccactagg cttcctttcc aggtcattgc ctctgatgca gggctactca cacaccgggt 1260
204 tcaaaccctca gatatgtatg ttgcagccgc agaacgtac gagattgtgt tcgatttcgc 1320
205 gccctatgcc ggccaaacgt tggatctgcg caacttcgca aaggccaatg gtatcggtac 1380
206 cgacgacgac tacgcaaaac ctgacaaggt catgcgtttc cagctcagca gccaaacagt 1440
207 cgtcgataac tccgtggtac ccgagcagct atctcagatc cagttccccg cggacaaaac 1500
208 cgacatagac catcacttcc gtttccatcg taccaacggc gattggcgca tcaacggcat 1560

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209 cggggtttgca gacgtcgaga accgtgttct tgccaaggta ccgcgcggta ctgtcgagct 1620
210 ttgggaactt gagaacagct ccggcggtcg gtcacacccc atccacgtcc acctagtaga 1680
211 cttccgagtc gtcgcacgct acggcgacga aggcactcgc ggcgtcatgc cctatgaggc 1740
212 cgccggtctc aaggacgtcg tgtggctcgg ccgtcacgag acgggtcctcg tcgaagcaca 1800
213 ttacgcccca tgggacggag tctacatgtt ccactgccac aaacctatcc acgaagacca 1860
214 agacatgatg gccgccttcg acgtgactaa actccagaac tttgggtaca acgagacgac 1920
215 tgatttccac gatcctgagg atcctcgcgt gtcagcaaga cctttcaccc cgggtgatct 1980
216 cacggcgcca tcgggtatct tttcagaaga atccatcagg gctagagtaa atgagttggc 2040
217 gctcgagcag ccttacagcg aactcgcaca agttacagcc tcgctcgagc agtactacaa 2100
218 gacgaaccag aaacgccacg acgagtgcga agacatgcct gctggcccta tccccgtta 2160
219 tcgtaggttt caggtctgat tcaagttgtt ttgggtgtgc aaattctcct tcttctctcc 2220
220 attgaactta attgtagatg atggatacac actcaattct cctttcttat ctcgacgctt 2280
221 tggccatttt atttggctct attgtgctat atactgtcta tttctctttc gtatacgagc 2340
222 aatgtatgtc ttggtcggag tcttgtggag ctgtcgaggt gacacctcgc gacgccatct 2400
223 tagcagtttt cgtaactctc gtctatttgt gattactttg ttccttaate agtaacagct 2460
224 tgatgttaga ttagcaatga gacgaacgat gaagcaatct gagatggatc cttttttttt 2520
225 cctaataattt gtatactaaa gaatgtgaac aatgccgttt tatgaaatgc tcataacatg 2580
226 cagcatattt actttgttct atttcatctt attttcatat gtacgcatac cctcggcatc 2640
227 agacaagaga cgcgacaacg ctctctgcat cccttctcgg ccgtaattc cgtagaaaat 2700
228 gaccgacggg aaagcagtc tccacgcgct ccatgctcat catgctcgt actatgtatc 2760
229 cccttccaac gcggatggcg cggatgtcgc tgcgaaccca ttgaatgggc atcacgacag 2820
230 ccatcatgtc gctaaggacg gattcttctt cggatgcaat gcttgtgagg gggttttctg 2880
231 catcccagca agatgaggtg gatcc 2905
233 <210> SEQ ID NO: 4
234 <211> LENGTH: 627
235 <212> TYPE: PRT
236 <213> ORGANISM: Bipolaris spicifera
238 <400> SEQUENCE: 4
239 Met Val Ala Lys Tyr Leu Phe Ser Ala Leu Gln Leu Val Ser Ile Ala
240 1 5 10 15
241 Lys Gly Ile Tyr Gly Val Ala Leu Ser Glu Arg Pro Ala Lys Phe Val
242 20 25 30
243 Asp Asn Thr Pro Asp Glu Glu Lys Ala Ala Leu Ala Ser Ile Val Glu
244 35 40 45
245 Asp Asp Pro Ala Asp Val Val Asn Met Leu Lys Asp Trp Gln Ser Pro
246 50 55 60
247 Glu Tyr Pro Leu Ile Phe Arg Gln Pro Leu Pro Ile Pro Pro Ala Lys
248 65 70 75 80
249 Glu Pro Asn Lys Leu Thr Asn Pro Val Thr Asn Lys Glu Ile Trp Tyr
250 85 90 95
251 Tyr Glu Ile Val Ile Lys Pro Phe Thr Gln Gln Val Tyr Pro Ser Leu
252 100 105 110
253 Arg Pro Ala Arg Leu Val Gly Tyr Asp Gly Ile Ser Pro Gly Pro Thr
254 115 120 125
255 Ile Ile Val Pro Arg Gly Thr Glu Ala Val Val Arg Phe Ile Asn Gln
256 130 135 140
257 Gly Asp Arg Glu Ser Ser Ile His Leu His Gly Ser Pro Ser Arg Ala
258 145 150 155 160
259 Pro Phe Asp Gly Trp Ala Asp Asp Met Ile Met Lys Gly Glu Tyr Lys

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Use of n and/or Aaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Yaa.

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:537 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:555 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:586 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:601 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:616 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:677 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17